

59419-010102.ST25.txt
SEQUENCE LISTING

<110> NG, Mary Mah Lee
Chu, Justin Jang Hann

<120> Molecules, Compositions, Methods and Kits For Applications
Associated With Flaviviruses

<130> 59419-010102

<140> to be assigned
<141> 2004-01-29

<150> US 60/442,157
<151> 2003-01-22

<150> To be assigned
<151> 2004-01-22

<160> 21

<170> PatentIn version 3.2

<210> 1
<211> 14
<212> PRT
<213> Vero cells

<220>
<221> misc_feature
<222> (10)..(10)
<223> Xaa can be any naturally occurring amino acid

<400> 1

Asp Thr Pro Lys Leu Glu Ile Ala Gly Xaa Phe Lys Asp Leu
1 5 10

<210> 2
<211> 14
<212> PRT
<213> Vero cells

<220>
<221> misc_feature
<222> (10)..(10)
<223> Xaa can be any naturally occurring amino acid

<400> 2

Ser Ile Pro Lys Leu Glu Ile Ala Gly Xaa Phe Lys Asp Leu
1 5 10

<210> 3
<211> 20
<212> PRT
<213> Vero cells

<400> 3

Met Tyr Ile Ser Pro Leu Glu Ala Leu Glu Gly Asn Pro Cys Tyr Asp
1 5 10 15

Met Lys Thr Cys
20

<210> 4
<211> 20
<212> PRT
<213> Vero cells

<400> 4

Val Val Ser Asp Asn His Tyr Ser Ala Ser Thr Thr Met Asp Tyr Pro
1 5 10 15

Leu Leu Gly Leu
20

<210> 5
<211> 20
<212> PRT
<213> Vero cells

<400> 5

Gln Gly Gln Leu Ile Ser Asp Gln Val Ala Glu Ile Ile Ser Lys Tyr
1 5 10 15

Asp Pro Asn Val
20

<210> 6
<211> 4
<212> PRT
<213> Synthetic peptide

<400> 6

Arg Phe Asp Ser
1

<210> 7
<211> 5
<212> PRT
<213> Synthetic peptide

<400> 7

Gly Arg Gly Asp Ser
1 5

<210> 8
<211> 3147

<212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> (1)..(3144)
 <223> Sequence coding for integrin alpha V subunit

<400> 8
 atg gct ttt ccg ccg cgg cga cgg ctg cgc ctc ggt ccc cgc ggc ctc 48
 Met Ala Phe Pro Pro Arg Arg Arg Leu Arg Leu Gly Pro Arg Gly Leu
 1 5 10 15
 ccg ctt ctt ctc tcg gga ctc ctg cta cct ctg tgc cgc gcc ttc aac 96
 Pro Leu Leu Leu Ser Gly Leu Leu Leu Pro Leu Cys Arg Ala Phe Asn
 20 25 30
 cta gac gtg gac agt cct gcc gag tac tct ggc ccc gag gga agt tac 144
 Leu Asp Val Asp Ser Pro Ala Glu Tyr Ser Gly Pro Glu Gly Ser Tyr
 35 40 45
 ttc ggc ttc gcc gtg gat ttc ttc gtg ccc agc gcg tct tcc cgg atg 192
 Phe Gly Phe Ala Val Asp Phe Phe Val Pro Ser Ala Ser Ser Arg Met
 50 55 60
 ttt ctt ctc gtg gga gct ccc aaa gca aac acc acc cag cct ggg att 240
 Phe Leu Leu Val Gly Ala Pro Lys Ala Asn Thr Thr Gln Pro Gly Ile
 65 70 75 80
 gtg gaa gga ggg cag gtc ctc aaa tgt gac tgg tct tct acc cgc cgg 288
 Val Glu Gly Gly Gln Val Leu Lys Cys Asp Trp Ser Ser Thr Arg Arg
 85 90 95
 tgc cag cca att gaa ttt gat gca aca ggc aat aga gat tat gcc aag 336
 Cys Gln Pro Ile Glu Phe Asp Ala Thr Gly Asn Arg Asp Tyr Ala Lys
 100 105 110
 gat gat cca ttg gaa ttt aag tcc cat cag tgg ttt gga gca tct gtg 384
 Asp Asp Pro Leu Glu Phe Lys Ser His Gln Trp Phe Gly Ala Ser Val
 115 120 125
 agg tcg aaa cag gat aaa att ttg gcc tgt gcc cca ttg tac cat tgg 432
 Arg Ser Lys Gln Asp Lys Ile Leu Ala Cys Ala Pro Leu Tyr His Trp
 130 135 140
 aga act gag atg aaa cag gag cga gag cct gtt gga aca tgc ttt ctt 480
 Arg Thr Glu Met Lys Gln Glu Arg Glu Pro Val Gly Thr Cys Phe Leu
 145 150 155 160
 caa gat gga aca aag act gtt gag tat gct cca tgt aga tca caa gat 528
 Gln Asp Gly Thr Lys Thr Val Glu Tyr Ala Pro Cys Arg Ser Gln Asp
 165 170 175
 att gat gct gat gga cag gga ttt tgt caa gga gga ttc agc att gat 576
 Ile Asp Ala Asp Gly Gln Gly Phe Cys Gln Gly Gly Phe Ser Ile Asp
 180 185 190
 ttt act aaa gct gac aga gta ctt ctt ggt ggt cct ggt agc ttt tat 624
 Phe Thr Lys Ala Asp Arg Val Leu Leu Gly Gly Pro Gly Ser Phe Tyr
 195 200 205
 tgg caa ggt cag ctt att tcg gat caa gtg gca gaa atc gta tct aaa 672

Trp	Gln	Gly	Gln	Leu	Ile	Ser	Asp	Gln	Val	Ala	Glu	Ile	Val	Ser	Lys	
210						215					220					
tac	gac	ccc	aat	gtt	tac	agc	atc	aag	tat	aat	aac	caa	tta	gca	act	720
Tyr	Asp	Pro	Asn	Val	Tyr	Ser	Ile	Lys	Tyr	Asn	Asn	Gln	Leu	Ala	Thr	
225					230					235					240	
cgg	act	gca	caa	gct	att	ttt	gat	gac	agc	tat	ttg	ggt	tat	tct	gtg	768
Arg	Thr	Ala	Gln	Ala	Ile	Phe	Asp	Asp	Ser	Tyr	Leu	Gly	Tyr	Ser	Val	
				245					250					255		
gct	gtc	gga	gat	ttc	aat	ggg	gat	ggc	ata	gat	gac	ttt	gtt	tca	gga	816
Ala	Val	Gly	Asp	Phe	Asn	Gly	Asp	Gly	Ile	Asp	Asp	Phe	Val	Ser	Gly	
			260					265					270			
gtt	cca	aga	gca	gca	agg	act	ttg	gga	atg	gtt	tat	att	tat	gat	ggg	864
Val	Pro	Arg	Ala	Ala	Arg	Thr	Leu	Gly	Met	Val	Tyr	Ile	Tyr	Asp	Gly	
		275					280					285				
aag	aac	atg	tcc	tcc	tta	tac	aat	ttt	act	ggc	gag	cag	atg	gct	gca	912
Lys	Asn	Met	Ser	Ser	Leu	Tyr	Asn	Phe	Thr	Gly	Glu	Gln	Met	Ala	Ala	
	290					295					300					
tat	ttc	gga	ttt	tct	gta	gct	gcc	act	gac	att	aat	gga	gat	gat	tat	960
Tyr	Phe	Gly	Phe	Ser	Val	Ala	Ala	Thr	Asp	Ile	Asn	Gly	Asp	Asp	Tyr	
305					310					315					320	
gca	gat	gtg	ttt	att	gga	gca	cct	ctc	ttc	atg	gat	cgt	ggc	tct	gat	1008
Ala	Asp	Val	Phe	Ile	Gly	Ala	Pro	Leu	Phe	Met	Asp	Arg	Gly	Ser	Asp	
				325					330					335		
ggc	aaa	ctc	caa	gag	gtg	ggg	cag	gtc	tca	gtg	tct	cta	cag	aga	gct	1056
Gly	Lys	Leu	Gln	Glu	Val	Gly	Gln	Val	Ser	Val	Ser	Leu	Gln	Arg	Ala	
			340					345					350			
tca	gga	gac	ttc	cag	acg	aca	aag	ctg	aat	gga	ttt	gag	gtc	ttt	gca	1104
Ser	Gly	Asp	Phe	Gln	Thr	Thr	Lys	Leu	Asn	Gly	Phe	Glu	Val	Phe	Ala	
		355					360					365				
cgg	ttt	ggc	agt	gcc	ata	gct	cct	ttg	gga	gat	ctg	gac	cag	gat	ggg	1152
Arg	Phe	Gly	Ser	Ala	Ile	Ala	Pro	Leu	Gly	Asp	Leu	Asp	Gln	Asp	Gly	
	370					375					380					
ttc	aat	gat	att	gca	att	gct	gct	cca	tat	ggg	ggg	gaa	gat	aaa	aaa	1200
Phe	Asn	Asp	Ile	Ala	Ile	Ala	Ala	Pro	Tyr	Gly	Gly	Glu	Asp	Lys	Lys	
385					390					395					400	
gga	att	gtt	tat	atc	ttc	aat	gga	aga	tca	aca	ggc	ttg	aac	gca	gtc	1248
Gly	Ile	Val	Tyr	Ile	Phe	Asn	Gly	Arg	Ser	Thr	Gly	Leu	Asn	Ala	Val	
				405					410					415		
cca	tct	caa	atc	ctt	gaa	ggg	cag	tgg	gct	gct	cga	agc	atg	cca	cca	1296
Pro	Ser	Gln	Ile	Leu	Glu	Gly	Gln	Trp	Ala	Ala	Arg	Ser	Met	Pro	Pro	
			420					425					430			
agc	ttt	ggc	tat	tca	atg	aaa	gga	gcc	aca	gat	ata	gac	aaa	aat	gga	1344
Ser	Phe	Gly	Tyr	Ser	Met	Lys	Gly	Ala	Thr	Asp	Ile	Asp	Lys	Asn	Gly	
		435					440					445				
tat	cca	gac	tta	att	gta	gga	gct	ttt	ggg	gta	gat	cga	gct	atc	tta	1392
Tyr	Pro	Asp	Leu	Ile	Val	Gly	Ala	Phe	Gly	Val	Asp	Arg	Ala	Ile	Leu	
	450					455					460					

59419-010102.ST25.txt

tac Tyr 465	agg Arg	gcc Ala	aga Arg	cca Pro	gtt Val 470	atc Ile	act Thr	gta Val	aat Asn	gct Ala 475	ggt Gly	ctt Leu	gaa Glu	gtg Val	tac Tyr 480	1440
cct Pro	agc Ser	att Ile	tta Leu	aat Asn 485	caa Gln	gac Asp	aat Asn	aaa Lys	acc Thr 490	tgc Cys	tca Ser	ctg Leu	cct Pro	gga Gly 495	aca Thr	1488
gct Ala	ctc Leu	aaa Lys	gtt Val 500	tcc Ser	tgt Cys	ttt Phe	aat Asn	gtt Val 505	agg Arg	ttc Phe	tgc Cys	tta Leu	aag Lys 510	gca Ala	gat Asp	1536
ggc Gly	aaa Lys	gga Gly 515	gta Val	ctt Leu	ccc Pro	agg Arg	aaa Lys 520	ctt Leu	aat Asn	ttc Phe	cag Gln	gtg Val 525	gaa Glu	ctt Leu	ctt Leu	1584
ttg Leu	gat Asp 530	aaa Lys	ctc Leu	aag Lys	caa Gln	aag Lys 535	gga Gly	gca Ala	att Ile	cga Arg	cga Arg 540	gca Ala	ctg Leu	ttt Phe	ctc Leu	1632
tac Tyr 545	agc Ser	agg Arg	tcc Ser	cca Pro	agt Ser 550	cac His	tcc Ser	aag Lys	aac Asn	atg Met 555	act Thr	att Ile	tca Ser	agg Arg	ggg Gly 560	1680
gga Gly	ctg Leu	atg Met	cag Gln	tgt Cys 565	gag Glu	gaa Glu	ttg Leu	ata Ile	gcg Ala 570	tat Tyr	ctg Leu	cgg Arg	gat Asp	gaa Glu 575	tct Ser	1728
gaa Glu	ttt Phe	aga Arg	gac Asp 580	aaa Lys	ctc Leu	act Thr	cca Pro	att Ile 585	act Thr	att Ile	ttt Phe	atg Met	gaa Glu 590	tat Tyr	cgg Arg	1776
ttg Leu	gat Asp	tat Tyr 595	aga Arg	aca Thr	gct Ala	gct Ala	gat Asp 600	aca Thr	aca Thr	ggc Gly	ttg Leu	caa Gln 605	ccc Pro	att Ile	ctt Leu	1824
aac Asn 610	cag Gln	ttc Phe	acg Thr	cct Pro	gct Ala	aac Asn 615	att Ile	agt Ser	cga Arg	cag Gln	gct Ala 620	cac His	att Ile	cta Leu	ctt Leu	1872
gac Asp 625	tgt Cys	ggt Gly	gaa Glu	gac Asp	aat Asn 630	gtc Val	tgt Cys	aaa Lys	ccc Pro	aag Lys 635	ctg Leu	gaa Glu	gtt Val	tct Ser	gta Val 640	1920
gat Asp	agt Ser	gat Asp	caa Gln	aag Lys 645	aag Lys	atc Ile	tat Tyr	att Ile	ggg Gly 650	gat Asp	gac Asp	aac Asn	cct Pro	ctg Leu 655	aca Thr	1968
ttg Leu	att Ile	gtt Val 660	aag Lys	gct Ala	cag Gln	aat Asn	caa Gln	gga Gly 665	gaa Glu	ggt Gly	gcc Ala	tac Tyr	gaa Glu 670	gct Ala	gag Glu	2016
ctc Leu	atc Ile	gtt Val 675	tcc Ser	att Ile	cca Pro	ctg Leu	cag Gln 680	gct Ala	gat Asp	ttc Phe	atc Ile	ggg Gly 685	gtt Val	gtc Val	cga Arg	2064
aac Asn 690	aat Asn	gaa Glu	gcc Ala	tta Leu	gca Ala	aga Arg 695	ctt Leu	tcc Ser	tgt Cys	gca Ala	ttt Phe 700	aag Lys	aca Thr	gaa Glu	aac Asn	2112
caa Gln 705	act Thr	cgc Arg	cag Gln	gtg Val 710	gta Val	tgt Cys	gac Asp	ctt Leu	gga Gly	aac Asn 715	cca Pro	atg Met	aag Lys	gct Ala	gga Gly 720	2160

59419-010102.ST25.txt

act	caa	ctc	tta	gct	ggt	ctt	cgt	ttc	agt	gtg	cac	cag	cag	tca	gag	2208
Thr	Gln	Leu	Leu	Ala	Gly	Leu	Arg	Phe	Ser	Val	His	Gln	Gln	Ser	Glu	
				725					730					735		
atg	gat	act	tct	gtg	aaa	ttt	gac	tta	caa	atc	caa	agc	tca	aat	cta	2256
Met	Asp	Thr	Ser	Val	Lys	Phe	Asp	Leu	Gln	Ile	Gln	Ser	Ser	Asn	Leu	
			740					745					750			
ttt	gac	aaa	gta	agc	cca	gtt	gta	tct	cac	aaa	gtt	gat	ctt	gct	gtt	2304
Phe	Asp	Lys	Val	Ser	Pro	Val	Val	Ser	His	Lys	Val	Asp	Leu	Ala	Val	
		755					760					765				
tta	gct	gca	gtt	gag	ata	aga	gga	gtc	tcg	agt	cct	gat	cat	atc	ttt	2352
Leu	Ala	Ala	Val	Glu	Ile	Arg	Gly	Val	Ser	Ser	Pro	Asp	His	Ile	Phe	
			770				775					780				
ctt	ccg	att	cca	aac	tgg	gag	cac	aag	gag	aac	cct	gag	act	gaa	gaa	2400
Leu	Pro	Ile	Pro	Asn	Trp	Glu	His	Lys	Glu	Asn	Pro	Glu	Thr	Glu	Glu	
					790					795					800	
gat	gtt	ggg	cca	gtt	gtt	cag	cac	atc	tat	gag	ctg	aga	aac	aat	ggt	2448
Asp	Val	Gly	Pro	Val	Val	Gln	His	Ile	Tyr	Glu	Leu	Arg	Asn	Asn	Gly	
				805					810					815		
cca	agt	tca	ttc	agc	aag	gca	atg	ctc	cat	ctt	cag	tgg	cct	tac	aaa	2496
Pro	Ser	Ser	Phe	Ser	Lys	Ala	Met	Leu	His	Leu	Gln	Trp	Pro	Tyr	Lys	
			820					825					830			
tat	aat	aat	aac	act	ctg	ttg	tat	atc	ctt	cat	tat	gat	att	gat	gga	2544
Tyr	Asn	Asn	Asn	Thr	Leu	Leu	Tyr	Ile	Leu	His	Tyr	Asp	Ile	Asp	Gly	
			835				840					845				
cca	atg	aac	tgc	act	tca	gat	atg	gag	atc	aac	cct	ttg	aga	att	aag	2592
Pro	Met	Asn	Cys	Thr	Ser	Asp	Met	Glu	Ile	Asn	Pro	Leu	Arg	Ile	Lys	
						855					860					
atc	tca	tct	ttg	caa	aca	act	gaa	aag	aat	gac	acg	gtt	gcc	ggg	caa	2640
Ile	Ser	Ser	Leu	Gln	Thr	Thr	Glu	Lys	Asn	Asp	Thr	Val	Ala	Gly	Gln	
					870					875					880	
ggt	gag	cgg	gac	cat	ctc	atc	act	aag	cgg	gat	ctt	gcc	ctc	agt	gaa	2688
Gly	Glu	Arg	Asp	His	Leu	Ile	Thr	Lys	Arg	Asp	Leu	Ala	Leu	Ser	Glu	
				885					890					895		
gga	gat	att	cac	act	ttg	ggt	tgt	gga	gtt	gct	cag	tgc	ttg	aag	att	2736
Gly	Asp	Ile	His	Thr	Leu	Gly	Cys	Gly	Val	Ala	Gln	Cys	Leu	Lys	Ile	
				900				905					910			
gtc	tgc	caa	gtt	ggg	aga	tta	gac	aga	gga	aag	agt	gca	atc	ttg	tac	2784
Val	Cys	Gln	Val	Gly	Arg	Leu	Asp	Arg	Gly	Lys	Ser	Ala	Ile	Leu	Tyr	
			915				920					925				
gta	aag	tca	tta	ctg	tgg	act	gag	act	ttt	atg	aat	aaa	gaa	aat	cag	2832
Val	Lys	Ser	Leu	Leu	Trp	Thr	Glu	Thr	Phe	Met	Asn	Lys	Glu	Asn	Gln	
					935						940					
aat	cat	tcc	tat	tct	ctg	aag	tcg	tct	gct	tca	ttt	aat	gtc	ata	gag	2880
Asn	His	Ser	Tyr	Ser	Leu	Lys	Ser	Ser	Ala	Ser	Phe	Asn	Val	Ile	Glu	
					950					955					960	
ttt	cct	tat	aag	aat	ctt	cca	att	gag	gat	atc	acc	aac	tcc	aca	ttg	2928
Phe	Pro	Tyr	Lys	Asn	Leu	Pro	Ile	Glu	Asp	Ile	Thr	Asn	Ser	Thr	Leu	

965

970

975

gtt acc act aat gtc acc tgg ggc att cag cca gcg ccc atg cct gtg 2976
 Val Thr Thr Asn Val Thr Trp Gly Ile Gln Pro Ala Pro Met Pro Val
 980 985 990

cct gtg tgg gtg atc att tta gca gtt cta gca gga ttg ttg cta ctg 3024
 Pro Val Trp Val Ile Ile Leu Ala Val Leu Ala Gly Leu Leu Leu Leu
 995 1000 1005

gct gtt ttg gta ttt gta atg tac agg atg ggc ttt ttt aaa cgg 3069
 Ala Val Leu Val Phe Val Met Tyr Arg Met Gly Phe Phe Lys Arg
 1010 1015 1020

gtc cgg cca cct caa gaa gaa caa gaa agg gag cag ctt caa cct 3114
 Val Arg Pro Pro Gln Glu Glu Gln Glu Arg Glu Gln Leu Gln Pro
 1025 1030 1035

cat gaa aat ggt gaa gga aac tca gaa act taa 3147
 His Glu Asn Gly Glu Gly Asn Ser Glu Thr
 1040 1045

<210> 9

<211> 1048

<212> PRT

<213> Homo Sapiens

<400> 9

Met Ala Phe Pro Pro Arg Arg Arg Leu Arg Leu Gly Pro Arg Gly Leu
 1 5 10 15

Pro Leu Leu Leu Ser Gly Leu Leu Leu Pro Leu Cys Arg Ala Phe Asn
 20 25 30

Leu Asp Val Asp Ser Pro Ala Glu Tyr Ser Gly Pro Glu Gly Ser Tyr
 35 40 45

Phe Gly Phe Ala Val Asp Phe Phe Val Pro Ser Ala Ser Ser Arg Met
 50 55 60

Phe Leu Leu Val Gly Ala Pro Lys Ala Asn Thr Thr Gln Pro Gly Ile
 65 70 75 80

Val Glu Gly Gly Gln Val Leu Lys Cys Asp Trp Ser Ser Thr Arg Arg
 85 90 95

Cys Gln Pro Ile Glu Phe Asp Ala Thr Gly Asn Arg Asp Tyr Ala Lys
 100 105 110

Asp Asp Pro Leu Glu Phe Lys Ser His Gln Trp Phe Gly Ala Ser Val
 115 120 125

Arg Ser Lys Gln Asp Lys Ile Leu Ala Cys Ala Pro Leu Tyr His Trp
 Page 7

130

135

Arg Thr Glu Met Lys Gln Glu Arg Glu Pro Val Gly Thr Cys Phe Leu
145 150 155 160

Gln Asp Gly Thr Lys Thr Val Glu Tyr Ala Pro Cys Arg Ser Gln Asp
165 170 175

Ile Asp Ala Asp Gly Gln Gly Phe Cys Gln Gly Gly Phe Ser Ile Asp
180 185 190

Phe Thr Lys Ala Asp Arg Val Leu Leu Gly Gly Pro Gly Ser Phe Tyr
195 200 205

Trp Gln Gly Gln Leu Ile Ser Asp Gln Val Ala Glu Ile Val Ser Lys
210 215 220

Tyr Asp Pro Asn Val Tyr Ser Ile Lys Tyr Asn Asn Gln Leu Ala Thr
225 230 235 240

Arg Thr Ala Gln Ala Ile Phe Asp Asp Ser Tyr Leu Gly Tyr Ser Val
245 250 255

Ala Val Gly Asp Phe Asn Gly Asp Gly Ile Asp Asp Phe Val Ser Gly
260 265 270

Val Pro Arg Ala Ala Arg Thr Leu Gly Met Val Tyr Ile Tyr Asp Gly
275 280 285

Lys Asn Met Ser Ser Leu Tyr Asn Phe Thr Gly Glu Gln Met Ala Ala
290 295 300

Tyr Phe Gly Phe Ser Val Ala Ala Thr Asp Ile Asn Gly Asp Asp Tyr
305 310 315 320

Ala Asp Val Phe Ile Gly Ala Pro Leu Phe Met Asp Arg Gly Ser Asp
325 330 335

Gly Lys Leu Gln Glu Val Gly Gln Val Ser Val Ser Leu Gln Arg Ala
340 345 350

Ser Gly Asp Phe Gln Thr Thr Lys Leu Asn Gly Phe Glu Val Phe Ala
355 360 365

Arg Phe Gly Ser Ala Ile Ala Pro Leu Gly Asp Leu Asp Gln Asp Gly
370 375 380

Phe Asn Asp Ile Ala Ile Ala Ala Pro Tyr Gly Gly Glu Asp Lys Lys
 385 390 395 400
 Gly Ile Val Tyr Ile Phe Asn Gly Arg Ser Thr Gly Leu Asn Ala Val
 405 410 415
 Pro Ser Gln Ile Leu Glu Gly Gln Trp Ala Ala Arg Ser Met Pro Pro
 420 425 430
 Ser Phe Gly Tyr Ser Met Lys Gly Ala Thr Asp Ile Asp Lys Asn Gly
 435 440 445
 Tyr Pro Asp Leu Ile Val Gly Ala Phe Gly Val Asp Arg Ala Ile Leu
 450 455 460
 Tyr Arg Ala Arg Pro Val Ile Thr Val Asn Ala Gly Leu Glu Val Tyr
 465 470 475 480
 Pro Ser Ile Leu Asn Gln Asp Asn Lys Thr Cys Ser Leu Pro Gly Thr
 485 490 495
 Ala Leu Lys Val Ser Cys Phe Asn Val Arg Phe Cys Leu Lys Ala Asp
 500 505 510
 Gly Lys Gly Val Leu Pro Arg Lys Leu Asn Phe Gln Val Glu Leu Leu
 515 520 525
 Leu Asp Lys Leu Lys Gln Lys Gly Ala Ile Arg Arg Ala Leu Phe Leu
 530 535 540
 Tyr Ser Arg Ser Pro Ser His Ser Lys Asn Met Thr Ile Ser Arg Gly
 545 550 555 560
 Gly Leu Met Gln Cys Glu Glu Leu Ile Ala Tyr Leu Arg Asp Glu Ser
 565 570 575
 Glu Phe Arg Asp Lys Leu Thr Pro Ile Thr Ile Phe Met Glu Tyr Arg
 580 585 590
 Leu Asp Tyr Arg Thr Ala Ala Asp Thr Thr Gly Leu Gln Pro Ile Leu
 595 600 605
 Asn Gln Phe Thr Pro Ala Asn Ile Ser Arg Gln Ala His Ile Leu Leu
 610 615 620
 Asp Cys Gly Glu Asp Asn Val Cys Lys Pro Lys Leu Glu Val Ser Val
 625 630 635 640

59419-010102.ST25.txt

Asp Ser Asp Gln Lys Lys Ile Tyr Ile Gly Asp Asp Asn Pro Leu Thr
 645 650 655
 Leu Ile Val Lys Ala Gln Asn Gln Gly Glu Gly Ala Tyr Glu Ala Glu
 660 665 670
 Leu Ile Val Ser Ile Pro Leu Gln Ala Asp Phe Ile Gly Val Val Arg
 675 680 685
 Asn Asn Glu Ala Leu Ala Arg Leu Ser Cys Ala Phe Lys Thr Glu Asn
 690 695 700
 Gln Thr Arg Gln Val Val Cys Asp Leu Gly Asn Pro Met Lys Ala Gly
 705 710 715 720
 Thr Gln Leu Leu Ala Gly Leu Arg Phe Ser Val His Gln Gln Ser Glu
 725 730 735
 Met Asp Thr Ser Val Lys Phe Asp Leu Gln Ile Gln Ser Ser Asn Leu
 740 745 750
 Phe Asp Lys Val Ser Pro Val Val Ser His Lys Val Asp Leu Ala Val
 755 760 765
 Leu Ala Ala Val Glu Ile Arg Gly Val Ser Ser Pro Asp His Ile Phe
 770 775 780
 Leu Pro Ile Pro Asn Trp Glu His Lys Glu Asn Pro Glu Thr Glu Glu
 785 790 795 800
 Asp Val Gly Pro Val Val Gln His Ile Tyr Glu Leu Arg Asn Asn Gly
 805 810 815
 Pro Ser Ser Phe Ser Lys Ala Met Leu His Leu Gln Trp Pro Tyr Lys
 820 825 830
 Tyr Asn Asn Asn Thr Leu Leu Tyr Ile Leu His Tyr Asp Ile Asp Gly
 835 840 845
 Pro Met Asn Cys Thr Ser Asp Met Glu Ile Asn Pro Leu Arg Ile Lys
 850 855 860
 Ile Ser Ser Leu Gln Thr Thr Glu Lys Asn Asp Thr Val Ala Gly Gln
 865 870 875 880
 Gly Glu Arg Asp His Leu Ile Thr Lys Arg Asp Leu Ala Leu Ser Glu
 885 890 895

Gly Asp Ile His Thr Leu Gly Cys Gly Val Ala Gln Cys Leu Lys Ile
900 905 910

Val Cys Gln Val Gly Arg Leu Asp Arg Gly Lys Ser Ala Ile Leu Tyr
915 920 925Val Lys Ser Leu Leu Trp Thr Glu Thr Phe Met Asn Lys Glu Asn Gln
930 935 940

Asn His Ser Tyr Ser Leu Lys Ser Ser Ala Ser Phe Asn Val Ile Glu
945 950 955 960

Phe Pro Tyr Lys Asn Leu Pro Ile Glu Asp Ile Thr Asn Ser Thr Leu
965 970 975

Val Thr Thr Asn Val Thr Trp Gly Ile Gln Pro Ala Pro Met Pro Val
980 985 990

Pro Val Trp Val Ile Ile Leu Ala Val Leu Ala Gly Leu Leu Leu Leu
995 1000 1005

Ala Val Leu Val Phe Val Met Tyr Arg Met Gly Phe Phe Lys Arg
1010 1015 1020

Val Arg Pro Pro Gln Glu Glu Gln Glu Arg Glu Gln Leu Gln Pro
1025 1030 1035

His Glu Asn Gly Glu Gly Asn Ser Glu Thr
1040 1045

<210>	10
<211>	2367
<212>	DNA
<213>	Homo Sapiens

```
<220>
<221> CDS
<222> (1)..(2364)
<223> Sequence coding for integrin beta 3 subunit
```

<400> 10
atg cga gcg cgg ccg cgg ccc cgg ccg ctc tgg gcg act gtg ctg gcg 48
Met Arg Ala Arg Pro Arg Pro Arg Pro Leu Trp Ala Thr Val Leu Ala
1 5 10 15

ctg ggg gcg ctg gcg ggc gtt ggc gta gga ggg ccc aac atc tgt acc 96
Leu Gly Ala Leu Ala Gly Val Gly Val Gly Gly Pro Asn Ile Cys Thr
20 25 30

acg cga ggt gtg agc tcc tgc cag cag tgc ctg gct gtg agc ccc atg 144
Page 11

59419-010102.ST25.txt

Thr	Arg	Gly	Val	Ser	Ser	Cys	Gln	Gln	Cys	Leu	Ala	Val	Ser	Pro	Met	
		35					40					45				
tgt	gcc	tgg	tgc	tct	gat	gag	gcc	ctg	cct	ctg	ggc	tca	cct	cg	tgt	192
Cys	Ala	Trp	Cys	Ser	Asp	Glu	Ala	Leu	Pro	Leu	Gly	Ser	Pro	Arg	Cys	
	50					55					60					
gac	ctg	aag	gag	aat	ctg	ctg	aag	gat	aac	tgt	gcc	cca	gaa	tcc	atc	240
Asp	Leu	Lys	Glu	Asn	Leu	Leu	Lys	Asp	Asn	Cys	Ala	Pro	Glu	Ser	Ile	
65					70					75					80	
gag	ttc	cca	gtg	agt	gag	gcc	cga	gta	cta	gag	gac	agg	ccc	ctc	agc	288
Glu	Phe	Pro	Val	Ser	Glu	Ala	Arg	Val	Leu	Glu	Asp	Arg	Pro	Leu	Ser	
				85					90					95		
gac	aag	ggc	tct	gga	gac	agc	tcc	cag	gtc	act	caa	gtc	agt	ccc	cag	336
Asp	Lys	Gly	Ser	Gly	Asp	Ser	Ser	Gln	Val	Thr	Gln	Val	Ser	Pro	Gln	
			100					105					110			
agg	att	gca	ctc	cgg	ctc	cgg	cca	gat	gat	tcg	aag	aat	ttc	tcc	atc	384
Arg	Ile	Ala	Leu	Arg	Leu	Arg	Pro	Asp	Asp	Ser	Lys	Asn	Phe	Ser	Ile	
		115					120					125				
caa	gtg	cgg	cag	gtg	gag	gat	tac	cct	gtg	gac	atc	tac	tac	ttg	atg	432
Gln	Val	Arg	Gln	Val	Glu	Asp	Tyr	Pro	Val	Asp	Ile	Tyr	Tyr	Leu	Met	
	130					135					140					
gac	ctg	tct	tac	tcc	atg	aag	gat	gat	ctg	tgg	agc	atc	cag	aac	ctg	480
Asp	Leu	Ser	Tyr	Ser	Met	Lys	Asp	Asp	Leu	Trp	Ser	Ile	Gln	Asn	Leu	
145					150					155					160	
ggg	acc	aag	ctg	gcc	acc	cag	atg	cga	aag	ctc	acc	agt	aac	ctg	cgg	528
Gly	Thr	Lys	Leu	Ala	Thr	Gln	Met	Arg	Lys	Leu	Thr	Ser	Asn	Leu	Arg	
				165					170					175		
att	ggc	ttc	ggg	gca	ttt	gtg	gac	aag	cct	gtg	tca	cca	tac	atg	tat	576
Ile	Gly	Phe	Gly	Ala	Phe	Val	Asp	Lys	Pro	Val	Ser	Pro	Tyr	Met	Tyr	
			180					185					190			
atc	tcc	cca	cca	gag	gcc	ctc	gaa	aac	ccc	tgc	tat	gat	atg	aag	acc	624
Ile	Ser	Pro	Pro	Glu	Ala	Leu	Glu	Asn	Pro	Cys	Tyr	Asp	Met	Lys	Thr	
		195					200					205				
acc	tgc	ttg	ccc	atg	ttt	ggc	tac	aaa	cac	gtg	ctg	acg	cta	act	gac	672
Thr	Cys	Leu	Pro	Met	Phe	Gly	Tyr	Lys	His	Val	Leu	Thr	Leu	Thr	Asp	
	210					215					220					
cag	gtg	acc	cgc	ttc	aat	gag	gaa	gtg	aag	aag	cag	agt	gtg	tca	cgg	720
Gln	Val	Thr	Arg	Phe	Asn	Glu	Glu	Val	Lys	Lys	Gln	Ser	Val	Ser	Arg	
225					230					235					240	
aac	cga	gat	gcc	cca	gag	ggg	ggc	ttt	gat	gcc	atc	atg	cag	gct	aca	768
Asn	Arg	Asp	Ala	Pro	Glu	Gly	Gly	Phe	Asp	Ala	Ile	Met	Gln	Ala	Thr	
				245					250					255		
gtc	tgt	gat	gaa	aag	att	ggc	tgg	agg	aat	gat	gca	tcc	cac	ttg	ctg	816
Val	Cys	Asp	Glu	Lys	Ile	Gly	Trp	Arg	Asn	Asp	Ala	Ser	His	Leu	Leu	
			260					265					270			
gtg	ttt	acc	act	gat	gcc	aag	act	cat	ata	gca	ttg	gac	gga	agg	ctg	864
Val	Phe	Thr	Thr	Asp	Ala	Lys	Thr	His	Ile	Ala	Leu	Asp	Gly	Arg	Leu	
		275					280					285				

59419-010102.ST25.txt

gca Ala 290	ggc Gly 290	att Ile	gtc Val	cag Gln	cct Pro	aat Asn 295	gac Asp	ggg Gly	cag Gln	tgt Cys	cat His 300	gtt Val	ggt Gly	agt Ser	gac Asp	912
aat Asn 305	cat His	tac Tyr	tct Ser	gcc Ala	tcc Ser 310	act Thr	acc Thr	atg Met	gat Asp	tat Tyr 315	ccc Pro	tct Ser	ttg Leu	ggg Gly	ctg Leu 320	960
atg Met	act Thr	gag Glu	aag Lys	cta Leu 325	tcc Ser	cag Gln	aaa Lys	aac Asn	atc Ile 330	aat Asn	ttg Leu	atc Ile	ttt Phe	gca Ala 335	gtg Val	1008
act Thr	gaa Glu	aat Asn	gta Val 340	gtc Val	aat Asn	ctc Leu	tat Tyr	cag Gln 345	aac Asn	tat Tyr	agt Ser	gag Glu	ctc Leu 350	atc Ile	cca Pro	1056
ggg Gly	acc Thr	aca Thr 355	gtt Val	ggg Gly	gtt Val	ctg Leu	tcc Ser 360	atg Met	gat Asp	tcc Ser	agc Ser	aat Asn 365	gtc Val	ctc Leu	cag Gln	1104
ctc Leu	att Ile 370	gtt Val	gat Asp	gct Ala	tat Tyr	ggg Gly 375	aaa Lys	atc Ile	cgt Arg	tct Ser	aaa Lys 380	gta Val	gag Glu	ctg Leu	gaa Glu	1152
gtg Val 385	cgt Arg	gac Asp	ctc Leu	cct Pro	gaa Glu 390	gag Glu	ttg Leu	tct Ser	cta Leu	tcc Ser 395	ttc Phe	aat Asn	gcc Ala	acc Thr	tgc Cys 400	1200
ctc Leu	aac Asn	aat Asn	gag Glu	gtc Val 405	atc Ile	cct Pro	ggc Gly	ctc Leu	aag Lys 410	tct Ser	tgt Cys	atg Met	gga Gly	ctc Leu 415	aag Lys	1248
att Ile	gga Gly	gac Asp	acg Thr 420	gtg Val	agc Ser	ttc Phe	agc Ser	att Ile 425	gag Glu	gcc Ala	aag Lys	gtg Val	cga Arg 430	ggc Gly	tgt Cys	1296
ccc Pro	cag Gln	gag Glu 435	aag Lys	gag Glu	aag Lys	tcc Ser	ttt Phe 440	acc Thr	ata Ile	aag Lys	ccc Pro	gtg Val 445	ggc Gly	ttc Phe	aag Lys	1344
gac Asp 450	agc Ser	ctg Leu	atc Ile	gtc Val	cag Gln	gtc Val 455	acc Thr	ttt Phe	gat Asp	tgt Cys	gac Asp 460	tgt Cys	gcc Ala	tgc Cys	cag Gln	1392
gcc Ala 465	caa Gln	gct Ala	gaa Glu	cct Pro	aat Asn 470	agc Ser	cat His	cgc Arg	tgc Cys	aac Asn 475	aat Asn	ggc Gly	aat Asn	ggg Gly	acc Thr 480	1440
ttt Phe	gag Glu	tgt Cys	ggg Gly	gta Val 485	tgc Cys	cgt Arg	tgt Cys	ggg Gly	cct Pro 490	ggc Gly	tgg Trp	ctg Leu	gga Gly	tcc Ser 495	cag Gln	1488
tgt Cys	gag Glu	tgc Cys	tca Ser 500	gag Glu	gag Glu	gac Asp	tat Tyr	cgc Arg 505	cct Pro	tcc Ser	cag Gln	cag Gln	gac Asp 510	gaa Glu	tgc Cys	1536
agc Ser	ccc Pro	cgg Arg 515	gag Glu	ggt Gly	cag Gln	ccc Pro	gtc Val 520	tgc Cys	agc Ser	cag Gln	cgg Arg 525	ggc Gly	gag Glu	tgc Cys	ctc Leu	1584
tgt Cys	ggt Gly 530	caa Gln	tgt Cys	gtc Val	tgc Cys	cac His 535	agc Ser	agt Ser	gac Asp	ttt Phe	ggc Gly 540	aag Lys	atc Ile	acg Thr	ggc Gly	1632

59419-010102.ST25.txt

aag Lys 545	tac Tyr	tgc Cys	gag Glu	tgt Cys	gac Asp 550	gac Asp	ttc Phe	tcc Ser	tgt Cys	gtc Val 555	cgc Arg	tac Tyr	aag Lys	ggg Gly	gag Glu 560	1680
atg Met	tgc Cys	tca Ser	ggc Gly	cat His 565	ggc Gly	cag Gln	tgc Cys	agc Ser	tgt Cys 570	ggg Gly	gac Asp	tgc Cys	ctg Leu	tgt Cys 575	gac Asp	1728
tcc Ser	gac Asp	tgg Trp	acc Thr 580	ggc Gly	tac Tyr	tac Tyr	tgc Cys	aac Asn 585	tgt Cys	acc Thr	acg Thr	cgt Arg	act Thr 590	gac Asp	acc Thr	1776
tgc Cys	atg Met	tcc Ser 595	agc Ser	aat Asn	ggg Gly	ctg Leu	ctg Leu 600	tgc Cys	agc Ser	ggc Gly	cgc Arg	ggc Gly 605	aag Lys	tgt Cys	gaa Glu	1824
tgt Cys	ggc Gly 610	agc Ser	tgt Cys	gtc Val	tgt Cys	atc Ile 615	cag Gln	ccg Pro	ggc Gly	tcc Ser	tat Tyr 620	ggg Gly	gac Asp	acc Thr	tgt Cys	1872
gag Glu 625	aag Lys	tgc Cys	ccc Pro	acc Thr	tgc Cys 630	cca Pro	gat Asp	gcc Ala	tgc Cys	acc Thr 635	ttt Phe	aag Lys	aaa Lys	gaa Glu	tgt Cys 640	1920
gtg Val	gag Glu	tgt Cys	aag Lys	aag Lys 645	ttt Phe	gac Asp	cgg Arg	gag Glu	ccc Pro 650	tac Tyr	atg Met	acc Thr	gaa Glu	aat Asn 655	acc Thr	1968
tgc Cys	aac Asn	cgt Arg	tac Tyr 660	tgc Cys	cgt Arg	gac Asp	gag Glu	att Ile 665	gag Glu	tca Ser	gtg Val	aaa Lys	gag Glu 670	ctt Leu	aag Lys	2016
gac Asp	act Thr	ggc Gly 675	aag Lys	gat Asp	gca Ala	gtg Val	aat Asn 680	tgt Cys	acc Thr	tat Tyr	aag Lys	aat Asn 685	gag Glu	gat Asp	gac Asp	2064
tgt Cys	gtc Val 690	gtc Val	aga Arg	ttc Phe	cag Gln	tac Tyr 695	tat Tyr	gaa Glu	gat Asp	tct Ser	agt Ser 700	gga Gly	aag Lys	tcc Ser	atc Ile	2112
ctg Leu 705	tat Tyr	gtg Val	gta Val	gaa Glu	gag Glu 710	cca Pro	gag Glu	tgt Cys	ccc Pro	aag Lys 715	ggc Gly	cct Pro	gac Asp	atc Ile	ctg Leu 720	2160
gtg Val	gtc Val	ctg Leu	ctc Leu	tca Ser 725	gtg Val	atg Met	ggg Gly	gcc Ala	att Ile 730	ctg Leu	ctc Leu	att Ile	ggc Gly	ctt Leu 735	gcc Ala	2208
gcc Ala	ctg Leu	ctc Leu	atc Ile 740	tgg Trp	aaa Lys	ctc Leu	ctc Leu	atc Ile 745	acc Thr	atc Ile	cac His	gac Asp	cga Arg 750	aaa Lys	gaa Glu	2256
ttc Phe	gct Ala	aaa Lys 755	ttt Phe	gag Glu	gaa Glu	gaa Glu	cgc Arg 760	gcc Ala	aga Arg	gca Ala	aaa Lys	tgg Trp 765	gac Asp	aca Thr	gcc Ala	2304
aac Asn 770	aac Asn	cca Pro	ctg Leu	tat Tyr	aaa Lys	gag Glu 775	gcc Ala	acg Thr	tct Ser	acc Thr	ttc Phe 780	acc Thr	aat Asn	atc Ile	acg Thr	2352
tac Tyr	cgg Arg	ggc Gly	act Thr	taa												2367

785

<210> 11
 <211> 788
 <212> PRT
 <213> Homo Sapiens

<400> 11

Met Arg Ala Arg Pro Arg Pro Arg Pro Leu Trp Ala Thr Val Leu Ala
 1 5 10 15

Leu Gly Ala Leu Ala Gly Val Gly Val Gly Gly Pro Asn Ile Cys Thr
 20 25 30

Thr Arg Gly Val Ser Ser Cys Gln Gln Cys Leu Ala Val Ser Pro Met
 35 40 45

Cys Ala Trp Cys Ser Asp Glu Ala Leu Pro Leu Gly Ser Pro Arg Cys
 50 55 60

Asp Leu Lys Glu Asn Leu Leu Lys Asp Asn Cys Ala Pro Glu Ser Ile
 65 70 75 80

Glu Phe Pro Val Ser Glu Ala Arg Val Leu Glu Asp Arg Pro Leu Ser
 85 90 95

Asp Lys Gly Ser Gly Asp Ser Ser Gln Val Thr Gln Val Ser Pro Gln
 100 105 110

Arg Ile Ala Leu Arg Leu Arg Pro Asp Asp Ser Lys Asn Phe Ser Ile
 115 120 125

Gln Val Arg Gln Val Glu Asp Tyr Pro Val Asp Ile Tyr Tyr Leu Met
 130 135 140

Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Trp Ser Ile Gln Asn Leu
 145 150 155 160

Gly Thr Lys Leu Ala Thr Gln Met Arg Lys Leu Thr Ser Asn Leu Arg
 165 170 175

Ile Gly Phe Gly Ala Phe Val Asp Lys Pro Val Ser Pro Tyr Met Tyr
 180 185 190

Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro Cys Tyr Asp Met Lys Thr
 195 200 205

Thr Cys Leu Pro Met Phe Gly Tyr Lys His Val Leu Thr Leu Thr Asp
 Page 15

210

215

Gln Val Thr Arg Phe Asn Glu Glu Val Lys Lys Gln Ser Val Ser Arg
225 230 235 240

Asn Arg Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr
245 250 255

Val Cys Asp Glu Lys Ile Gly Trp Arg Asn Asp Ala Ser His Leu Leu
260 265 270

Val Phe Thr Thr Asp Ala Lys Thr His Ile Ala Leu Asp Gly Arg Leu
275 280 285

Ala Gly Ile Val Gln Pro Asn Asp Gly Gln Cys His Val Gly Ser Asp
290 295 300

Asn His Tyr Ser Ala Ser Thr Thr Met Asp Tyr Pro Ser Leu Gly Leu
305 310 315 320

Met Thr Glu Lys Leu Ser Gln Lys Asn Ile Asn Leu Ile Phe Ala Val
325 330 335

Thr Glu Asn Val Val Asn Leu Tyr Gln Asn Tyr Ser Glu Leu Ile Pro
340 345 350

Gly Thr Thr Val Gly Val Leu Ser Met Asp Ser Ser Asn Val Leu Gln
355 360 365

Leu Ile Val Asp Ala Tyr Gly Lys Ile Arg Ser Lys Val Glu Leu Glu
370 375 380

Val Arg Asp Leu Pro Glu Glu Leu Ser Leu Ser Phe Asn Ala Thr Cys
385 390 395 400

Leu Asn Asn Glu Val Ile Pro Gly Leu Lys Ser Cys Met Gly Leu Lys
405 410 415

Ile Gly Asp Thr Val Ser Phe Ser Ile Glu Ala Lys Val Arg Gly Cys
420 425 430

Pro Gln Glu Lys Glu Lys Ser Phe Thr Ile Lys Pro Val Gly Phe Lys
435 440 445

Asp Ser Leu Ile Val Gln Val Thr Phe Asp Cys Asp Cys Ala Cys Gln
450 455 460

Ala Gln Ala Glu Pro Asn Ser His Arg Cys Asn Asn Gly Asn Gly Thr
 465 470 475 480

Phe Glu Cys Gly Val Cys Arg Cys Gly Pro Gly Trp Leu Gly Ser Gln
 485 490 495

Cys Glu Cys Ser Glu Glu Asp Tyr Arg Pro Ser Gln Gln Asp Glu Cys
 500 505 510

Ser Pro Arg Glu Gly Gln Pro Val Cys Ser Gln Arg Gly Glu Cys Leu
 515 520 525

Cys Gly Gln Cys Val Cys His Ser Ser Asp Phe Gly Lys Ile Thr Gly
 530 535 540

Lys Tyr Cys Glu Cys Asp Asp Phe Ser Cys Val Arg Tyr Lys Gly Glu
 545 550 555 560

Met Cys Ser Gly His Gly Gln Cys Ser Cys Gly Asp Cys Leu Cys Asp
 565 570 575

Ser Asp Trp Thr Gly Tyr Tyr Cys Asn Cys Thr Thr Arg Thr Asp Thr
 580 585 590

Cys Met Ser Ser Asn Gly Leu Leu Cys Ser Gly Arg Gly Lys Cys Glu
 595 600 605

Cys Gly Ser Cys Val Cys Ile Gln Pro Gly Ser Tyr Gly Asp Thr Cys
 610 615 620

Glu Lys Cys Pro Thr Cys Pro Asp Ala Cys Thr Phe Lys Lys Glu Cys
 625 630 635 640

Val Glu Cys Lys Lys Phe Asp Arg Glu Pro Tyr Met Thr Glu Asn Thr
 645 650 655

Cys Asn Arg Tyr Cys Arg Asp Glu Ile Glu Ser Val Lys Glu Leu Lys
 660 665 670

Asp Thr Gly Lys Asp Ala Val Asn Cys Thr Tyr Lys Asn Glu Asp Asp
 675 680 685

Cys Val Val Arg Phe Gln Tyr Tyr Glu Asp Ser Ser Gly Lys Ser Ile
 690 695 700

Leu Tyr Val Val Glu Glu Pro Glu Cys Pro Lys Gly Pro Asp Ile Leu
 705 710 715 720

Val Val Leu Leu Ser Val Met Gly Ala Ile Leu Leu Ile Gly Leu Ala
 725 730 735

Ala Leu Leu Ile Trp Lys Leu Leu Ile Thr Ile His Asp Arg Lys Glu
 740 745 750

Phe Ala Lys Phe Glu Glu Glu Arg Ala Arg Ala Lys Trp Asp Thr Ala
 755 760 765

Asn Asn Pro Leu Tyr Lys Glu Ala Thr Ser Thr Phe Thr Asn Ile Thr
 770 775 780

Tyr Arg Gly Thr
 785

<210> 12
 <211> 64
 <212> DNA
 <213> Synthetic DNA

<220>
 <221> misc_feature
 <222> (1)..(64)
 <223> Integrin sequence alpha v1

<400> 12
 gatcccgga ttgtttatat cttcattcaa gagatgaaga tataaacaat tccttttttg 60
 gaaa 64

<210> 13
 <211> 64
 <212> DNA
 <213> Synthetic DNA

<220>
 <221> misc_feature
 <222> (1)..(64)
 <223> Integrin sequence alpha v2

<400> 13
 gatcccgact ttcctgtgca tttaattcaa gagattaaat gcacaggaaa gtcttttttg 60
 gaaa 64

<210> 14
 <211> 63
 <212> DNA
 <213> Synthetic DNA

<220>
 <221> misc_feature

<222> (1)..(63)

<223> Integrin sequence beta 31

<400> 14

gatccacat caatttgatc tttgcttcaa gagagcaaag atcaaattga tgttttttgg 60

aaa

63

<210> 15

<211> 64

<212> DNA

<213> Synthetic DNA

<220>

<221> misc_feature

<222> (1)..(64)

<223> Integrin sequence beta 32

<400> 15

gatccgttgt acctataaga atgagttcaa gagactcatt cttataggta caattttttg 60

gaaa

64

<210> 16

<211> 1233

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1233)

<223> Sequence coding for neurotensin receptor

<400> 16

atg	gaa	acc	agc	agc	ccg	cgg	ccc	ccg	cgg	ccc	agc	tcc	aac	ccg	ggg	48
Met	Glu	Thr	Ser	Ser	Pro	Arg	Pro	Pro	Arg	Pro	Ser	Ser	Asn	Pro	Gly	
1				5					10					15		

ctg	agc	ctg	gac	gcc	cgg	ctg	ggc	gtg	gac	act	cgc	ctc	tgg	gcc	aag	96
Leu	Ser	Leu	Asp	Ala	Arg	Leu	Gly	Val	Asp	Thr	Arg	Leu	Trp	Ala	Lys	
			20				25						30			

gtg	ctg	ttc	acc	gcg	ctc	tac	gca	ctc	atc	tgg	gcg	ctg	ggc	gcg	gcg	144
Val	Leu	Phe	Thr	Ala	Leu	Tyr	Ala	Leu	Ile	Trp	Ala	Leu	Gly	Ala	Ala	
		35					40					45				

ggc	aat	gcg	ctg	tcc	gtg	cac	gtg	gtg	ctg	aag	gcg	cgg	gcc	ggg	cgc	192
Gly	Asn	Ala	Leu	Ser	Val	His	Val	Val	Leu	Lys	Ala	Arg	Ala	Gly	Arg	
	50					55					60					

gcg	ggg	cgc	ctg	cgc	cac	gtg	ctc	agc	ctg	gcg	ctc	gcg	ggc	ctg		240
Ala	Gly	Arg	Leu	Arg	His	Val	Leu	Ser	Leu	Ala	Leu	Ala	Gly	Leu		
65					70				75					80		

ctg	ctg	ctg	ctg	gtc	ggc	gtg	ccg	gtg	gag	ctc	tac	agc	ttc	gtg	tgg	288
Leu	Leu	Leu	Leu	Val	Gly	Val	Pro	Val	Glu	Leu	Tyr	Ser	Phe	Val	Trp	
				85					90					95		

ttc	cac	tac	ccc	tgg	gtc	ttc	ggc	gac	ctg	ggc	tgc	cgc	ggc	tac	tac	336
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Phe	His	Tyr	Pro 100	Trp	Val	Phe	Gly	Asp 105	Leu	Gly	Cys	Arg	Gly 110	Tyr	Tyr	
ttc	gtg	cac	gag	ctg	tgc	gcc	tac	gcc	acg	gtg	ctg	agc	gtg	gca	ggc	384
Phe	Val	His 115	Glu	Leu	Cys	Ala	Tyr 120	Ala	Thr	Val	Leu	Ser 125	Val	Ala	Gly	
ctg	agc	gcc	gag	cgc	tgc	cta	gcc	gtg	tgc	cag	ccc	ctg	cgt	gcc	cgc	432
Leu	Ser 130	Ala	Glu	Arg	Cys	Leu 135	Ala	Val	Cys	Gln	Pro 140	Leu	Arg	Ala	Arg	
agc	ctg	ctg	acg	cca	cgc	cgg	acc	cgg	tgg	ctg	gtg	gcg	ctc	tcg	tgg	480
Ser 145	Leu	Leu	Thr	Pro	Arg 150	Arg	Thr	Arg	Trp	Leu 155	Val	Ala	Leu	Ser	Trp 160	
gcc	gcc	tcg	ctc	ggc	ctc	gcc	ctg	ccc	atg	gcc	gtc	atc	atg	ggg	cag	528
Ala	Ala	Ser	Leu	Gly 165	Leu	Ala	Leu	Pro	Met 170	Ala	Val	Ile	Met	Gly 175	Gln	
aag	cac	gaa	ctc	gag	acg	gcg	gac	ggg	gag	ccg	gag	ccc	gcc	tcg	cga	576
Lys	His	Glu	Leu 180	Glu	Thr	Ala	Asp	Gly 185	Glu	Pro	Glu	Pro	Ala 190	Ser	Arg	
gtg	tgc	acg	gtg	ctg	gtg	agc	cgc	acc	gcg	ctc	caa	gtc	ttt	atc	cag	624
Val	Cys	Thr 195	Val	Leu	Val	Ser	Arg 200	Thr	Ala	Leu	Gln	Val 205	Phe	Ile	Gln	
gtg	aat	gtg	ctg	gtg	tcc	ttc	gtg	ctc	ccc	ttg	gca	cta	act	gct	ttc	672
Val	Asn 210	Val	Leu	Val	Ser	Phe 215	Val	Leu	Pro	Leu	Ala 220	Leu	Thr	Ala	Phe	
ctg	aat	ggg	gtc	aca	gtg	agc	cac	ctg	ctg	gcc	ctc	tgc	tcc	caa	gtg	720
Leu	Asn	Gly	Val	Thr	Val 230	Ser	His	Leu	Leu	Ala 235	Leu	Cys	Ser	Gln	Val 240	
ccg	tcc	act	tct	acc	ccg	ggc	agc	tcc	acc	ccc	agc	cgc	ctg	gag	ctg	768
Pro	Ser	Thr	Ser	Thr 245	Pro	Gly	Ser	Ser	Thr 250	Pro	Ser	Arg	Leu	Glu 255	Leu	
ctg	agt	gag	gag	ggc	ctc	ctc	agc	ttc	atc	gta	tgg	aag	aag	acc	ttt	816
Leu	Ser	Glu	Glu 260	Gly	Leu	Leu	Ser	Phe 265	Ile	Val	Trp	Lys	Lys 270	Thr	Phe	
atc	cag	gga	ggc	cag	gtc	agc	ctg	gtg	aga	cat	aaa	gac	gtg	cgc	cgg	864
Ile	Gln	Gly 275	Gly	Gln	Val	Ser	Leu 280	Val	Arg	His	Lys	Asp 285	Val	Arg	Arg	
atc	cgc	agc	ctc	cag	cgc	agc	gtc	cag	gtt	ctc	aga	gcc	atc	gtg	gtc	912
Ile	Arg 290	Ser	Leu	Gln	Arg	Ser 295	Val	Gln	Val	Leu	Arg 300	Ala	Ile	Val	Val	
atg	tat	gtc	atc	tgc	tgg	ctg	ccg	tac	cat	gcc	cgc	agg	ctc	atg	tac	960
Met	Tyr	Val	Ile	Cys	Trp 310	Leu	Pro	Tyr	His	Ala 315	Arg	Arg	Leu	Met	Tyr 320	
tgc	tac	gta	cct	gat	gac	gcg	tgg	act	gac	cca	ctg	tac	aat	ttc	tac	1008
Cys	Tyr	Val	Pro	Asp 325	Asp	Ala	Trp	Thr	Asp 330	Pro	Leu	Tyr	Asn	Phe 335	Tyr	
cac	tac	ttc	tac	atg	gtg	acc	aac	aca	ctt	ttc	tac	gtc	agc	tca	gct	1056
His	Tyr	Phe	Tyr 340	Met	Val	Thr	Asn	Thr 345	Leu	Phe	Tyr	Val	Ser 350	Ser	Ala	

59419-010102.ST25.txt

gtg	act	cct	ctt	ctc	tac	aac	gcc	gtg	tcc	tcc	tcc	ttc	aga	aaa	ctc	1104
Val	Thr	Pro	Leu	Leu	Tyr	Asn	Ala	Val	Ser	Ser	Ser	Phe	Arg	Lys	Leu	
		355					360					365				
ttc	ctg	gaa	gcc	gtc	agc	tcc	ctg	tgt	gga	gag	cac	cac	ccc	atg	aag	1152
Phe	Leu	Glu	Ala	Val	Ser	Ser	Leu	Cys	Gly	Glu	His	His	Pro	Met	Lys	
	370					375					380					
cgg	tta	ccc	ccg	aag	ccc	cag	agt	ccc	acc	cta	atg	gat	aca	gct	tca	1200
Arg	Leu	Pro	Pro	Lys	Pro	Gln	Ser	Pro	Thr	Leu	Met	Asp	Thr	Ala	Ser	
385					390					395					400	
ggc	ttt	ggg	gat	ccc	cca	gaa	acc	cgg	acc	tga						1233
Gly	Phe	Gly	Asp	Pro	Pro	Glu	Thr	Arg	Thr							
				405					410							

<210> 17
 <211> 410
 <212> PRT
 <213> Homo sapiens

<400> 17

Met	Glu	Thr	Ser	Ser	Pro	Arg	Pro	Pro	Arg	Pro	Ser	Ser	Asn	Pro	Gly	
1				5					10					15		
Leu	Ser	Leu	Asp	Ala	Arg	Leu	Gly	Val	Asp	Thr	Arg	Leu	Trp	Ala	Lys	
			20					25					30			
Val	Leu	Phe	Thr	Ala	Leu	Tyr	Ala	Leu	Ile	Trp	Ala	Leu	Gly	Ala	Ala	
		35					40					45				
Gly	Asn	Ala	Leu	Ser	Val	His	Val	Val	Leu	Lys	Ala	Arg	Ala	Gly	Arg	
	50					55					60					
Ala	Gly	Arg	Leu	Arg	His	His	Val	Leu	Ser	Leu	Ala	Leu	Ala	Gly	Leu	
65					70				75						80	
Leu	Leu	Leu	Leu	Val	Gly	Val	Pro	Val	Glu	Leu	Tyr	Ser	Phe	Val	Trp	
				85					90					95		
Phe	His	Tyr	Pro	Trp	Val	Phe	Gly	Asp	Leu	Gly	Cys	Arg	Gly	Tyr	Tyr	
			100					105					110			
Phe	Val	His	Glu	Leu	Cys	Ala	Tyr	Ala	Thr	Val	Leu	Ser	Val	Ala	Gly	
		115					120					125				
Leu	Ser	Ala	Glu	Arg	Cys	Leu	Ala	Val	Cys	Gln	Pro	Leu	Arg	Ala	Arg	
	130					135					140					
Ser	Leu	Leu	Thr	Pro	Arg	Arg	Thr	Arg	Trp	Leu	Val	Ala	Leu	Ser	Trp	
145					150					155					160	

59419-010102.ST25.txt

Ala Ala Ser Leu Gly Leu Ala Leu Pro Met Ala Val Ile Met Gly Gln
165 170 175

Lys His Glu Leu Glu Thr Ala Asp Gly Glu Pro Glu Pro Ala Ser Arg
180 185 190

Val Cys Thr Val Leu Val Ser Arg Thr Ala Leu Gln Val Phe Ile Gln
195 200 205

Val Asn Val Leu Val Ser Phe Val Leu Pro Leu Ala Leu Thr Ala Phe
210 215 220

Leu Asn Gly Val Thr Val Ser His Leu Leu Ala Leu Cys Ser Gln Val
225 230 235 240

Pro Ser Thr Ser Thr Pro Gly Ser Ser Thr Pro Ser Arg Leu Glu Leu
245 250 255

Leu Ser Glu Glu Gly Leu Leu Ser Phe Ile Val Trp Lys Lys Thr Phe
260 265 270

Ile Gln Gly Gly Gln Val Ser Leu Val Arg His Lys Asp Val Arg Arg
275 280 285

Ile Arg Ser Leu Gln Arg Ser Val Gln Val Leu Arg Ala Ile Val Val
290 295 300

Met Tyr Val Ile Cys Trp Leu Pro Tyr His Ala Arg Arg Leu Met Tyr
305 310 315 320

Cys Tyr Val Pro Asp Asp Ala Trp Thr Asp Pro Leu Tyr Asn Phe Tyr
325 330 335

His Tyr Phe Tyr Met Val Thr Asn Thr Leu Phe Tyr Val Ser Ser Ala
340 345 350

Val Thr Pro Leu Leu Tyr Asn Ala Val Ser Ser Ser Phe Arg Lys Leu
355 360 365

Phe Leu Glu Ala Val Ser Ser Leu Cys Gly Glu His His Pro Met Lys
370 375 380

Arg Leu Pro Pro Lys Pro Gln Ser Pro Thr Leu Met Asp Thr Ala Ser
385 390 395 400

Gly Phe Gly Asp Pro Pro Glu Thr Arg Thr
405 410

<210> 18
 <211> 65
 <212> DNA
 <213> Synthetic DNA

<220>
 <221> misc_feature
 <222> (1)..(65)
 <223> Functional sequence of neurotensin receptor used for siRNA

<400> 18
 gatcccgta tgacttttgg acagtcttca agagagactg tccaaaagtc ataatttttt 60
 ggaaa 65

<210> 19
 <211> 14
 <212> PRT
 <213> West Nile Virus

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> Xaa can be any naturally occurring amino acid

<400> 19
 Ser Ile Pro Lys Leu Glu Ile Ala Gly Xaa Phe Lys Asp Leu
 1 5 10

<210> 20
 <211> 1520
 <212> DNA
 <213> West Nile Virus

<220>
 <221> misc_feature
 <222> (1)..(11)
 <223> Primer sequence

<220>
 <221> CDS
 <222> (12)..(1520)
 <223> Sequence coding for the Domain III portion of the Envelope protein

<400> 20
 cggaattcag c ttc aac tgt tta gga atg agc aac agg gac ttc ctg gag 50
 Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu
 1 5 10

gga gtg tct gga gct aca tgg gtt gat ctg gta ctg gaa gga gac agt 98
 Gly Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser
 15 20 25

tgt gtg acc ata atg tca aaa gac aag cca acc att gat gtc aaa atg 146
 Page 23

59419-010102.ST25.txt

Cys 30	Val	Thr	Ile	Met	Ser 35	Lys	Asp	Lys	Pro	Thr 40	Ile	Asp	Val	Lys	Met 45	
atg Met	aac Asn	atg Met	gaa Glu	gca Ala 50	gct Ala	aat Asn	ctc Leu	gca Ala	gat Asp 55	gtg Val	cgt Arg	agc Ser	tac Tyr	tgc Cys 60	tac Tyr	194
tta Leu	gct Ala	tcg Ser	gtc Val 65	agt Ser	gat Asp	ctg Leu	tca Ser	aca Thr 70	aaa Lys	gcc Ala	gcg Ala	tgt Cys 75	cca Pro	acc Thr	atg Met	242
ggt Gly	gaa Glu	gct Ala 80	cac His	aac Asn	gag Glu	aaa Lys	aga Arg 85	gcc Ala	gac Asp	cct Pro	gcc Ala	ttt Phe 90	gtt Val	tgc Cys	aag Lys	290
caa Gln	ggc Gly 95	gtc Val	gta Val	gac Asp	aga Arg	gga Gly 100	tgg Trp	ggg Gly	aat Asn	gga Gly 105	tgc Cys	gga Gly	ctg Leu	ttt Phe	gga Gly	338
aag Lys 110	ggg Gly	agc Ser	att Ile	gac Asp	aca Thr 115	tgt Cys	gca Ala	aag Lys	ttt Phe	gcc Ala 120	tgt Cys	aca Thr	acc Thr	aag Lys	gca Ala 125	386
act Thr	ggt Gly	tgg Trp	att Ile	atc Ile 130	cag Gln	aag Lys	gaa Glu	aac Asn	atc Ile 135	aag Lys	tac Tyr	gag Glu	gtt Val	gcc Ala 140	ata Ile	434
ttt Phe	gtg Val	cat His	ggc Gly 145	ccg Pro	acg Thr	act Thr	gtc Val	gaa Glu 150	tca Ser	cat His	ggc Gly	aat Asn	tat Tyr 155	tca Ser	aca Thr	482
cag Gln	ata Ile	ggg Gly 160	gct Ala	acc Thr	caa Gln	gca Ala	gga Gly 165	agg Arg	ttc Phe	agc Ser	ata Ile	act Thr 170	cca Pro	tcg Ser	gca Ala	530
cca Pro	tcc Ser 175	tac Tyr	acg Thr	ctg Leu	aag Lys	ttg Leu 180	ggt Gly	gag Glu	tat Tyr	ggt Gly 185	gag Glu	gtc Val	aca Thr	gtt Val	gac Asp	578
tgt Cys 190	gag Glu	cca Pro	cgg Arg	tca Ser	gga Gly 195	ata Ile	gac Asp	act Thr	agc Ser	gct Ala 200	tac Tyr	tac Tyr	gtt Val	atg Met	tca Ser 205	626
gtg Val	ggt Gly	gcg Ala	aag Lys	tcc Ser 210	ttc Phe	ttg Leu	gtt Val	cac His	cga Arg 215	gaa Glu	tgg Trp	ttt Phe	atg Met	gac Asp 220	ctg Leu	674
aac Asn	ctt Leu	cca Pro	tgg Trp 225	agt Ser	agc Ser	gct Ala	gga Gly	agc Ser 230	aca Thr	acg Thr	tgg Trp	agg Arg	aac Asn 235	cgg Arg	gaa Glu	722
aca Thr	ctg Leu	atg Met 240	gag Glu	ttt Phe	gaa Glu	gaa Glu	cct Pro 245	cat His	gcc Ala	acc Thr	aaa Lys	caa Gln 250	tct Ser	gtc Val	gta Val	770
gct Ala	cta Leu 255	ggg Gly	tcg Ser	cag Gln	gaa Glu	ggt Gly 260	gcc Ala	ttg Leu	cac His	caa Gln	gct Ala 265	ctg Leu	gct Ala	gga Gly	gca Ala	818
att Ile 270	cct Pro	gtt Val	gag Glu	ttc Phe	tca Ser 275	agc Ser	aac Asn	act Thr	gtg Val	aag Lys 280	ttg Leu	aca Thr	tca Ser	gga Gly	cat His 285	866

59419-010102.ST25.txt

ctg aag tgt agg gtg aag atg gag aag ttg cag ctg aag gga aca aca	914
Leu Lys Cys Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr	
	290
	295
	300
tat ggt gta tgc tca aaa gca ttc aaa ttc gct agg act ccc gct gac	962
Tyr Gly Val Cys Ser Lys Ala Phe Lys Phe Ala Arg Thr Pro Ala Asp	
	305
	310
	315
act ggt cat gga acg gtg gtg ctg gaa ctg cag tat acc gga aaa gac	1010
Thr Gly His Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Lys Asp	
	320
	325
	330
ggg cct tgc aaa gtg ccc att tct tct gtg gct tcc ctg aac gac ctt	1058
Gly Pro Cys Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu	
	335
	340
	345
aca ccc gtt gga agg ctg gtg act gtg aat cca ttt gtg tct gtg gct	1106
Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala	
	350
	355
	360
acg gcc aac tcg aag gtt ttg att gaa ctc gaa ccc ccg ttt agt gac	1154
Thr Ala Asn Ser Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Ser Asp	
	370
	375
	380
tct tac atc gtg gtg ggg aga gga gaa cag cag ata aac cac cac tgg	1202
Ser Tyr Ile Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp	
	385
	390
	395
cac aaa tct ggg agc agt att gga aag gct ttc acc act aca ctc aga	1250
His Lys Ser Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Arg	
	400
	405
	410
gga gct caa cga ctt gca gct ctt gga gac act gcc tgg gat ttt gga	1298
Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly	
	415
	420
	425
tca gtc gga ggg gtt ttc acc tcg gta ggg aaa gcc ata cac caa gtt	1346
Ser Val Gly Gly Val Phe Thr Ser Val Gly Lys Ala Ile His Gln Val	
	430
	435
	440
	445
ttt gga gga gcc ttt aga tca ctc ttt gga ggg atg tcc tgg atc aca	1394
Phe Gly Gly Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr	
	450
	455
	460
cag ggg ctt ctg gga gct ctt ctg ctg tgg atg gga att aac gcc cgt	1442
Gln Gly Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg	
	465
	470
	475
gac agg tca att gct atg acg ttc ctt gcg gtt gga gga gtc ttg ctc	1490
Asp Arg Ser Ile Ala Met Thr Phe Leu Ala Val Gly Gly Val Leu Leu	
	480
	485
	490
ttc ctt tcg gtc aac gtc cat gct gga tcc	1520
Phe Leu Ser Val Asn Val His Ala Gly Ser	
	495
	500

<210> 21
 <211> 503
 <212> PRT
 <213> west Nile virus
 <400> 21

59419-010102.ST25.txt

Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser
 1 5 10 15
 Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr
 20 25 30
 Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met
 35 40 45
 Glu Ala Ala Asn Leu Ala Asp Val Arg Ser Tyr Cys Tyr Leu Ala Ser
 50 55 60
 Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala
 65 70 75 80
 His Asn Glu Lys Arg Ala Asp Pro Ala Phe Val Cys Lys Gln Gly Val
 85 90 95
 Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
 100 105 110
 Ile Asp Thr Cys Ala Lys Phe Ala Cys Thr Thr Lys Ala Thr Gly Trp
 115 120 125
 Ile Ile Gln Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His
 130 135 140
 Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Ile Gly
 145 150 155 160
 Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ser Ala Pro Ser Tyr
 165 170 175
 Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro
 180 185 190
 Arg Ser Gly Ile Asp Thr Ser Ala Tyr Tyr Val Met Ser Val Gly Ala
 195 200 205
 Lys Ser Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro
 210 215 220
 Trp Ser Ser Ala Gly Ser Thr Thr Trp Arg Asn Arg Glu Thr Leu Met
 225 230 235 240
 Glu Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Val Ala Leu Gly
 245 250 255

Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val
 260 265 270
 Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys
 275 280 285
 Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val
 290 295 300
 Cys Ser Lys Ala Phe Lys Phe Ala Arg Thr Pro Ala Asp Thr Gly His
 305 310 315 320
 Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Lys Asp Gly Pro Cys
 325 330 335
 Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val
 340 345 350
 Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn
 355 360 365
 Ser Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Ser Asp Ser Tyr Ile
 370 375 380
 Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser
 385 390 395 400
 Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Arg Gly Ala Gln
 405 410 415
 Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly
 420 425 430
 Gly Val Phe Thr Ser Val Gly Lys Ala Ile His Gln Val Phe Gly Gly
 435 440 445
 Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu
 450 455 460
 Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser
 465 470 475 480
 Ile Ala Met Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser
 485 490 495
 Val Asn Val His Ala Gly Ser

500

59419-010102.ST25.txt